

REMARKS

In compliance with the requirements of 37 C.F.R. §§ 1.821-1.825, the paper and computer readable copies of the Sequence Listing are enclosed herewith.

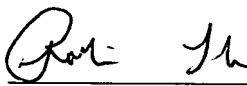
In accordance with 37 C.F.R. § 1.821(f) , Applicant's undersigned representative hereby declares that the content of the paper and computer readable copies are the same.

In accordance with 37 C.F.R. § 1.821(g), applicant's undersigned representative hereby declares that this submission contains now new matter.

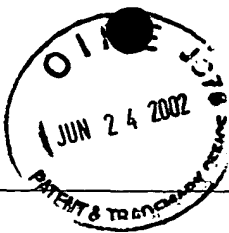
It is believed that this application is now in condition for examination. Early notice to this effect is respectfully requested.

Respectfully submitted,
Pillsbury Winthrop LLP

Date: June 24, 2002

By: 
Robin L. Teskin
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RECEIVED

SEQUENCE LISTING

JUN 26 2002

TECH CENTER 1600/2900

(1) GENERAL INFORMATION:

(i) APPLICANT: Anderson, Darrell R.

(ii) TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
- (B) STREET: 699 Prince Street
- (C) CITY: Alexandria
- (D) STATE: VA
- (E) COUNTRY: USA
- (F) ZIP: 22314

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/487,550
- (B) FILING DATE: 07-JUN-1995
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Teskin, Robin L.
- (B) REGISTRATION NUMBER: 35,030
- (C) REFERENCE/DOCKET NUMBER: 012712-131

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 703 836 6620
- (B) TELEFAX: 703 836 2021

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..705

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG	AGG	GTC	CCC	GCT	CAG	CTC	CTG	GGG	CTC	CTG	CTG	CTC	TGG	CTC	CCA	48
Met	Arg	Val	Pro	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Pro	
1				5				10					15			
GGT	GCA	CGA	TGT	GCC	TAT	GAA	CTG	ACT	CAG	CCA	CCC	TCG	GTG	TCA	GTG	96
Gly	Ala	Arg	Cys	Ala	Tyr	Glu	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Val	
			20					25					30			
TCC	CCA	GGA	CAG	ACG	GCC	AGG	ATC	ACC	TGT	GGG	GGA	GAC	AAC	AGT	AGA	144
Ser	Pro	Gly	Gln	Thr	Ala	Arg	Ile	Thr	Cys	Gly	Gly	Asp	Asn	Ser	Arg	
		35					40					45				
AAT	GAA	TAT	GTC	CAC	TGG	TAC	CAG	CAG	AAG	CCA	GCG	CGG	GCC	CCT	ATA	192
Asn	Glu	Tyr	Val	His	Trp	Tyr	Gln	Gln	Lys	Pro	Ala	Arg	Ala	Pro	Ile	
	50					55				60						
CTG	GTC	ATC	TAT	GAT	GAT	AGT	GAC	CGG	CCC	TCA	GGG	ATC	CCT	GAG	CGA	240
Leu	Val	Ile	Tyr	Asp	Asp	Ser	Asp	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	
65				70				75						80		
TTC	TCT	GGC	TCC	AAA	TCA	GGG	AAC	ACC	GCC	ACC	CTG	ACC	ATC	AAC	GGG	288
Phe	Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Asn	Gly	
				85				90						95		
GTC	GAG	GCC	GGG	GAT	GAG	GCT	GAC	TAT	TAC	TGT	CAG	GTG	TGG	GAC	AGG	336
Val	Glu	Ala	Gly	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Arg	
			100					105					110			
GCT	AGT	GAT	CAT	CCG	GTC	TTC	GGA	GGA	GGG	ACC	CGG	GTG	ACC	GTC	CTA	384
Ala	Ser	Asp	His	Pro	Val	Phe	Gly	Gly	Gly	Thr	Arg	Val	Thr	Val	Leu	
		115					120					125				
GGT	CAG	CCC	AAG	GCT	GCC	CCC	TCG	GTC	ACT	CTG	TTC	CCG	CCC	TCC	TCT	432
Gly	Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	
	130					135					140					
GAG	GAG	CTT	CAA	GCC	AAC	AAG	GCC	ACA	CTG	GTG	TGT	CTC	ATA	AGT	GAC	480
Glu	Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp	
145				150				155						160		
TTC	TAC	CCG	GGA	GCC	GTG	ACA	GTG	GCC	TGG	AAG	GCA	GAT	AGC	AGC	CCC	528
Phe	Tyr	Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	Ala	Asp	Ser	Ser	Pro	
			165					170						175		
GTC	AAG	GCG	GGA	GTG	GAG	ACC	ACC	ACA	CCC	TCC	AAA	CAA	AGC	AAC	AAC	576
Val	Lys	Ala	Gly	Val	Glu	Thr	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	Asn	

180										185					190					
AAG	TAC	GCG	GCC	AGC	AGC	TAC	CTG	AGC	CTG	ACG	CCT	GAG	CAG	TGG	AAG	624				
Lys	Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys					
		195					200					205								
TCC	CAC	AGA	AGC	TAC	AGC	TGC	CAG	GTC	ACG	CAT	GAA	GGG	AGC	ACC	GTG	672				
Ser	His	Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val					
		210				215					220									
GAG	AAG	ACA	GTG	GCC	CCT	ACA	GAA	TGT	TCA	TGA						705				
Glu	Lys	Thr	Val	Ala	Pro	Thr	Glu	Cys	Ser	*										
225					230					235										

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp Leu Pro
 1 5 10 15
 Gly Ala Arg Cys Ala Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val
 20 25 30
 Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asp Asn Ser Arg
 35 40 45
 Asn Glu Tyr Val His Trp Tyr Gln Gln Lys Pro Ala Arg Ala Pro Ile
 50 55 60
 Leu Val Ile Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg
 65 70 75 80
 Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Thr Leu Thr Ile Asn Gly
 85 90 95
 Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg
 100 105 110
 Ala Ser Asp His Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu
 115 120 125
 Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
 130 135 140
 Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
 145 150 155 160

Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
 165 170 175
 Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
 180 185 190
 Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
 195 200 205
 Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
 210 215 220
 Glu Lys Thr Val Ala Pro Thr Glu Cys Ser *
 225 230 235

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1431 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..1431

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..1431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCT CCC AGA TGG	48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp	
1 5 10 15	
GTC CTG TCC CAG GTG AAG CTG CAG CAG TGG GGC GAA GGA CTT CTG CAG	96
Val Leu Ser Gln Val Lys Leu Gln Gln Trp Gly Glu Gly Leu Leu Gln	
20 25 30	
CCT TCG GAG ACC CTG TCC CGC ACC TGC GTT GTC TCT GGT GGC TCC ATC	144
Pro Ser Glu Thr Leu Ser Arg Thr Cys Val Val Ser Gly Gly Ser Ile	
35 40 45	
AGC GGT TAC TAC TAC TGG ACC TGG ATC CGC CAG ACC CCA GGG AGG GGA	192
Ser Gly Tyr Tyr Tyr Trp Thr Trp Ile Arg Gln Thr Pro Gly Arg Gly	
50 55 60	
CTG GAG TGG ATT GGC CAT ATT TAT GGT AAT GGT GCG ACC ACC AAC TAC	240
Leu Glu Trp Ile Gly His Ile Tyr Gly Asn Gly Ala Thr Thr Asn Tyr	
65 70 75 80	

AAT Asn	CCC Pro	TCC Ser	CTC Leu	AAG Lys 85	AGT Ser	CGA Arg	GTC Val	ACC Thr	ATT Ile 90	TCA Ser	AAA Lys	GAC Asp	ACG Thr	TCC Ser 95	AAG Lys	288
AAC Asn	CAG Gln	TTC Phe 100	TTC Phe 100	CTG Leu	AAC Asn	TTG Leu	AAT Asn	TCT Ser 105	GTG Val	ACC Thr	GAC Asp	GCG Ala 110	GAC Asp 110	ACG Thr	GCC Ala	336
GTC Val	TAT Tyr 115	TAC Tyr 115	TGT Cys	GCG Ala	AGA Arg	GGC Gly	CCT Pro 120	CGC Arg	CCT Pro	GAT Asp	TGC Cys 125	ACA Thr 125	ACC Thr	ATT Ile	TGT Cys	384
TAT Tyr 130	GGC Gly 130	GGC Gly	TGG Trp	GTC Val	GAT Asp	GTC Val 135	TGG Trp	GGC Gly	CCG Pro	GGA Gly 140	GAC Asp 140	CTG Leu	GTC Val	ACC Thr	GTC Val	432
TCC Ser 145	TCA Ser	GCT Ala	AGC Ser	ACC Thr	AAG Lys 150	GGC Gly	CCA Pro	TCG Ser	GTC Val	TTC Phe 155	CCC Pro	CTG Leu	GCA Ala	CCC Pro	TCC Ser 160	480
TCC Ser	AAG Lys	AGC Ser	ACC Thr	TCT Ser 165	GGG Gly	GGC Gly	ACA Thr	GCG Ala	GCC Ala 170	CTG Leu	GGC Gly	TGC Cys	CTG Leu	GTC Val 175	AAG Lys	528
GAC Asp	TAC Tyr	TTC Phe 180	CCC Pro	GAA Glu	CCG Pro	GTG Val	ACG Thr	GTG Val 185	TCG Ser	TGG Trp	AAC Asn	TCA Ser	GGC Gly 190	GCC Ala	CTG Leu	576
ACC Thr	AGC Ser	GGC Gly 195	GTG Val	CAC His	ACC Thr	TTC Phe	CCG Pro 200	GCT Ala	GTC Val	CTA Leu	CAG Gln	TCC Ser 205	TCA Ser	GGA Gly	CTC Leu	624
TAC Tyr 210	TCC Ser	CTC Leu	AGC Ser	AGC Ser	GTG Val	GTG Val 215	ACC Thr	GTG Val	CCC Pro	TCC Ser 220	AGC Ser	AGC Ser	TTG Leu	GGC Gly	ACC Thr	672
CAG Gln 225	ACC Thr	TAC Tyr	ATC Ile	TGC Cys	AAC Asn 230	GTG Val	AAT Asn	CAC His	AAG Lys	CCC Pro 235	AGC Ser	AAC Asn	ACC Thr	AAG Lys	GTG Val 240	720
GAC Asp	AAG Lys	AAA Lys	GCA Ala	GAG Glu 245	CCC Pro	AAA Lys	TCT Ser	TGT Cys	GAC Asp 250	AAA Lys	ACT Thr	CAC His	ACA Thr	TGC Cys 255	CCA Pro	768
CCG Pro	TGC Cys	CCA Pro	GCA Ala 260	CCT Pro	GAA Glu	CTC Leu	CTG Leu	GGG Gly 265	GGA Gly	CCG Pro	TCA Ser	GTC Val	TTC Phe 270	CTC Leu	TTC Phe	816
CCC Pro	CCA Pro	AAA Lys 275	CCC Pro	AAG Lys	GAC Asp	ACC Thr	CTC Leu 280	ATG Met	ATC Ile	TCC Ser	CGG Arg	ACC Thr 285	CCT Pro	GAG Glu	GTC Val	864
ACA Thr 290	TGC Cys	GTG Val	GTG Val	GTG Val	GAC Asp	GTG Val 295	AGC Ser	CAC His	GAA Glu	GAC Asp	CCT Pro 300	GAG Glu	GTC Val	AAG Lys	TTC Phe	912

AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG	960
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro	
305 310 315 320	
CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC	1008
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr	
325 330 335	
GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC	1056
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val	
340 345 350	
TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC	1104
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala	
355 360 365	
AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG	1152
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg	
370 375 380	
GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC	1200
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly	
385 390 395 400	
TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG	1248
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro	
405 410 415	
GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC	1296
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser	
420 425 430	
TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG	1344
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln	
435 440 445	
GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC	1392
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His	
450 455 460	
TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA	1431
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys *	
465 470 475	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 1 5 10 15
 Val Leu Ser Gln Val Lys Leu Gln Gln Trp Gly Glu Gly Leu Leu Gln
 20 25 30
 Pro Ser Glu Thr Leu Ser Arg Thr Cys Val Val Ser Gly Gly Ser Ile
 35 40 45
 Ser Gly Tyr Tyr Tyr Trp Thr Trp Ile Arg Gln Thr Pro Gly Arg Gly
 50 55 60
 Leu Glu Trp Ile Gly His Ile Tyr Gly Asn Gly Ala Thr Thr Asn Tyr
 65 70 75 80
 Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Thr Ser Lys
 85 90 95
 Asn Gln Phe Phe Leu Asn Leu Asn Ser Val Thr Asp Ala Asp Thr Ala
 100 105 110
 Val Tyr Tyr Cys Ala Arg Gly Pro Arg Pro Asp Cys Thr Thr Ile Cys
 115 120 125
 Tyr Gly Gly Trp Val Asp Val Trp Gly Pro Gly Asp Leu Val Thr Val
 130 135 140
 Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
 145 150 155 160
 Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
 165 170 175
 Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
 180 185 190
 Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
 195 200 205
 Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
 210 215 220
 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
 225 230 235 240
 Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 245 250 255
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 260 265 270
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 275 280 285
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 290 295 300

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 305 310 315 320
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 325 330 335
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 340 345 350
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 355 360 365
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 370 375 380
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 385 390 395 400
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 405 410 415
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 420 425 430
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 435 440 445
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 450 455 460
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys *
 465 470 475

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..720

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG AGC CTC CCT GCT CAG CTC CTC GGG CTG CTA TTG CTC TGC GTC CCC

Met 1	Ser	Leu	Pro	Ala 5	Gln	Leu	Leu	Gly	Leu 10	Leu	Leu	Leu	Cys	Val 15	Pro	
GGG Gly	TCC Ser	AGT Ser	GGG Gly 20	GAA Glu	GTT Val	GTG Val	ATG Met	ACT Thr 25	CAG Gln	TCT Ser	CCA Pro	CTG Leu	TCC Ser 30	CTT Leu	CCC Pro	96
ATC Ile	ACA Thr	CCT Pro 35	GGA Gly	GAG Glu	CCG Pro	GCC Ala	TCC Ser 40	ATC Ile	TCC Ser	TGT Cys	AGG Arg	TCT Ser 45	AGT Ser	CAA Gln	AGC Ser	144
CTT Leu	AAA Lys 50	CAC His	AGT Ser	AAT Asn	GGA Gly	GAC Asp 55	ACC Thr	TTC Phe	CTG Leu	AGT Ser	TGG Trp 60	TAT Tyr	CAG Gln	CAG Gln	AAG Lys	192
CCA Pro 65	GGC Gly	CAA Gln	CCT Pro	CCA Pro	AGG Arg 70	CTC Leu	CTG Leu	ATT Ile	TAT Tyr	AAG Lys 75	GTT Val	TCT Ser	AAC Asn	CGG Arg	GAC Asp 80	240
TCT Ser	GGG Gly	GTC Val	CCA Pro	GAC Asp 85	AGA Arg	TTC Phe	AGC Ser	GGC Gly 90	AGT Ser	GGG Gly	GCA Ala	GGG Gly	ACA Thr	GAT Asp 95	TTC Phe	288
ACA Thr	CTG Leu	AAA Lys 100	ATC Ile	AGC Ser	GCA Ala	GTG Val	GAG Glu	GCT Ala 105	GAA Glu	GAT Asp	GTT Val	GGG Gly 110	GTT Val	TAT Tyr	TTC Phe	336
TGC Cys	GGG Gly	CAA Gln 115	GGT Gly	ACA Thr	AGG Arg	ACT Thr	CCT Pro 120	CCC Pro	ACT Thr	TTC Phe	GGC Gly	GGA Gly 125	GGG Gly	ACC Thr	AAG Lys	384
GTG Val 130	GAA Glu	ATC Ile	AAA Lys	CGT Arg	ACG Thr	GTG Val 135	GCT Ala	GCA Ala	CCA Pro	TCT Ser	GTC Val 140	TTC Phe	ATC Ile	TTC Phe	CCG Pro	432
CCA Pro 145	TCT Ser	GAT Asp	GAG Glu	CAG Gln	TTG Leu 150	AAA Lys	TCT Ser	GGA Gly	ACT Thr	GCC Ala 155	TCT Ser	GTT Val	GTG Val	TGC Cys	CTG Leu 160	480
CTG Leu	AAT Asn	AAC Asn	TTC Phe 165	TAT Tyr	CCC Pro	AGA Arg	GAG Glu	GCC Ala 170	AAA Lys	GTA Val	CAG Gln	TGG Trp	AAG Lys 175	GTG Val	GAT Asp	528
AAC Asn	GCC Ala	CTC Leu 180	CAA Gln	TCG Ser	GGT Gly	AAC Asn	TCC Ser	CAG Gln 185	GAG Glu	AGT Ser	GTC Val	ACA Thr	GAG Glu 190	CAG Gln	GAC Asp	576
AGC Ser	AAG Lys	GAC Asp 195	AGC Ser	ACC Thr	TAC Tyr	AGC Ser	CTC Leu 200	AGC Ser	AGC Ser	ACC Thr	CTG Leu 205	ACG Thr	CTG Leu	AGC Ser	AAA Lys	624
GCA Ala 210	GAC Asp	TAC Tyr	GAG Glu	AAA Lys	CAC His	AAA Lys 215	GTC Val	TAC Tyr	GCC Ala	TGC Cys	GAA Glu 220	GTC Val	ACC Thr	CAT His	CAG Gln	672
GGC	CTG	AGC	TCG	CCC	GTC	ACA	AAG	AGC	TTC	AAC	AGG	GGA	GAG	TGT	TGA	720

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *
 225 230 235 240

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ser Leu Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Cys Val Pro
 1 5 10 15
 Gly Ser Ser Gly Glu Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
 20 25 30
 Ile Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
 35 40 45
 Leu Lys His Ser Asn Gly Asp Thr Phe Leu Ser Trp Tyr Gln Gln Lys
 50 55 60
 Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Asp
 65 70 75 80
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe
 85 90 95
 Thr Leu Lys Ile Ser Ala Val Glu Ala Glu Asp Val Gly Val Tyr Phe
 100 105 110
 Cys Gly Gln Gly Thr Arg Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys
 115 120 125
 Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
 130 135 140
 Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
 145 150 155 160
 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
 165 170 175
 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
 180 185 190
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
 195 200 205
 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
 210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *
 225 230 235 240

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1437

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GGT TGG AGC CTC ATC TTG CTC TTC CTT GTC GCT GTT GCT ACG CGT 48
 Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg
 1 5 10 15

GTC CAG TGT GAG GTG CAA CTG GTG GAG TCT GGG GGA GGC TTG GTC CAG 96
 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 20 25 30

CCT GGC GGG TCC CTG AGA GTC TCC TGT GCA GTC TCT GGA TTC ACC TTC 144
 Pro Gly Gly Ser Leu Arg Val Ser Cys Ala Val Ser Gly Phe Thr Phe
 35 40 45

AGT GAC CAC TAC ATG TAT TGG TTC CGC CAG GCT CCA GGG AAG GGG CCG 192
 Ser Asp His Tyr Met Tyr Trp Phe Arg Gln Ala Pro Gly Lys Gly Pro
 50 55 60

GAA TGG GTA GGT TTC ATT AGA AAC AAA CCG AAC GGT GGG ACA ACA GAA 240
 Glu Trp Val Gly Phe Ile Arg Asn Lys Pro Asn Gly Gly Thr Thr Glu
 65 70 75 80

TAC GCC GCG TCT GTG AAA GAC AGA TTC ACC ATC TCC AGA GAT GAT TCC 288
 Tyr Ala Ala Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
 85 90 95

AAA AGC ATC GCC TAT CTG CAA ATG AGC AGC CTG AAA ATC GAG GAC ACG 336
 Lys Ser Ile Ala Tyr Leu Gln Met Ser Ser Leu Lys Ile Glu Asp Thr
 100 105 110

GCC GTC TAT TAC TGT ACT ACA TCC TAC ATT TCA CAT TGT CGG GGT GGT 384
 Ala Val Tyr Tyr Cys Thr Thr Ser Tyr Ile Ser His Cys Arg Gly Gly

115					120					125						
GTC Val	TGC Cys 130	TAT Tyr	GGA Gly	GGT Gly	TAC Tyr	TTC Phe 135	GAA Glu	TTC Phe	TGG Trp	GGC Gly	CAG Gln 140	GGC Gly	GCC Ala	CTG Leu	GTC Val	432
ACC Thr 145	GTC Val	TCC Ser	TCA Ser	GCT Ala	AGC Ser 150	ACC Thr	AAG Lys	GGC Gly	CCA Pro	TCG Ser 155	GTC Val	TTC Phe	CCC Pro	CTG Leu	GCA Ala 160	480
CCC Pro	TCC Ser	TCC Ser	AAG Lys	AGC Ser 165	ACC Thr	TCT Ser	GGG Gly	GGC Gly	ACA Thr 170	GCG Ala	GCC Ala	CTG Leu	GGC Gly	TGC Cys 175	CTG Leu	528
GTC Val	AAG Lys	GAC Asp	TAC Tyr 180	TTC Phe	CCC Pro	GAA Glu	CCG Pro	GTG Val 185	ACG Thr	GTG Val	TCG Ser	TGG Trp	AAC Asn 190	TCA Ser	GGC Gly	576
GCC Ala	CTG Leu	ACC Thr 195	AGC Ser	GGC Gly	GTG Val	CAC His	ACC Thr 200	TTC Phe	CCG Pro	GCT Ala	GTC Val	CTA Leu 205	CAG Gln	TCC Ser	TCA Ser	624
GGA Gly	CTC Leu 210	TAC Tyr	TCC Ser	CTC Leu	AGC Ser	AGC Ser 215	GTG Val	GTG Val	ACC Thr	GTG Val	CCC Pro 220	TCC Ser	AGC Ser	AGC Ser	TTG Leu	672
GGC Gly 225	ACC Thr	CAG Gln	ACC Thr	TAC Tyr	ATC Ile 230	TGC Cys	AAC Asn	GTG Val	AAT Asn	CAC His 235	AAG Lys	CCC Pro	AGC Ser	AAC Asn	ACC Thr 240	720
AAG Lys	GTG Val	GAC Asp	AAG Lys	AAA Lys 245	GCA Ala	GAG Glu	CCC Pro	AAA Lys	TCT Ser 250	TGT Cys	GAC Asp	AAA Lys	ACT Thr	CAC His 255	ACA Thr	768
TGC Cys	CCA Pro	CCG Pro	TGC Cys 260	CCA Pro	GCA Ala	CCT Pro	GAA Glu	CTC Leu 265	CTG Leu	GGG Gly	GGA Gly	CCG Pro	TCA Ser 270	GTC Val	TTC Phe	816
CTC Leu	TTC Phe	CCC Pro 275	CCA Pro	AAA Lys	CCC Pro	AAG Lys	GAC Asp 280	ACC Thr	CTC Leu	ATG Met	ATC Ile	TCC Ser 285	CGG Arg	ACC Thr	CCT Pro	864
GAG Glu	GTC Val 290	ACA Thr	TGC Cys	GTG Val	GTG Val	GTG Val 295	GAC Asp	GTG Val	AGC Ser	CAC His	GAA Glu 300	GAC Asp	CCT Pro	GAG Glu	GTC Val	912
AAG Lys 305	TTC Phe	AAC Asn	TGG Trp	TAC Tyr	GTG Val 310	GAC Asp	GGC Gly	GTG Val	GAG Glu	GTG Val 315	CAT His	AAT Asn	GCC Ala	AAG Lys	ACA Thr 320	960
AAG Lys	CCG Pro	CGG Arg	GAG Glu	GAG Glu	CAG Gln 325	TAC Tyr	AAC Asn	AGC Ser	ACG Thr 330	TAC Tyr	CGT Arg	GTG Val	GTC Val	AGC Ser 335	GTC Val	1008
CTC Leu	ACC Thr	GTC Val	CTG Leu	CAC His	CAG Gln	GAC Asp	TGG Trp	CTG Leu	AAT Asn	GGC Gly	AAG Lys	GAG Glu	TAC Tyr	AAG Lys	TGC Cys	1056

340						345						350						
AAG Lys	GTC Val	TCC Ser	AAC Asn	AAA Lys	GCC Ala	CTC Leu	CCA Pro	GCC Ala	CCC Pro	ATC Ile	GAG Glu	AAA Lys	ACC Thr	ATC Ile	TCC Ser	1104		
355						360						365						
AAA Lys	GCC Ala	AAA Lys	GGG Gly	CAG Gln	CCC Pro	CGA Arg	GAA Glu	CCA Pro	CAG Gln	GTG Val	TAC Tyr	ACC Thr	CTG Leu	CCC Pro	CCA Pro	1152		
370						375						380						
TCC Ser	CGG Arg	GAT Asp	GAG Glu	CTG Leu	ACC Thr	AAG Lys	AAC Asn	CAG Gln	GTC Val	AGC Ser	CTG Leu	ACC Thr	TGC Cys	CTG Leu	GTC Val	1200		
385						390						395					400	
AAA Lys	GGC Gly	TTC Phe	TAT Tyr	CCC Pro	AGC Ser	GAC Asp	ATC Ile	GCC Ala	GTG Val	GAG Glu	TGG Trp	GAG Glu	AGC Ser	AAT Asn	GGG Gly	1248		
405						410						415						
CAG Gln	CCG Pro	GAG Glu	AAC Asn	AAC Asn	TAC Tyr	AAG Lys	ACC Thr	ACG Thr	CCT Pro	CCC Pro	GTG Val	CTG Leu	GAC Asp	TCC Ser	GAC Asp	1296		
420						425						430						
GGC Gly	TCC Ser	TTC Phe	TTC Phe	CTC Leu	TAC Tyr	AGC Ser	AAG Lys	CTC Leu	ACC Thr	GTG Val	GAC Asp	AAG Lys	AGC Ser	AGG Arg	TGG Trp	1344		
435						440						445						
CAG Gln	CAG Gln	GGG Gly	AAC Asn	GTC Val	TTC Phe	TCA Ser	TGC Cys	TCC Ser	GTG Val	ATG Met	CAT His	GAG Glu	GCT Ala	CTG Leu	CAC His	1392		
450						455						460						
AAC Asn	CAC His	TAC Tyr	ACG Thr	CAG Gln	AAG Lys	AGC Ser	CTC Leu	TCC Ser	CTG Leu	TCT Ser	CCG Pro	GGT Gly	AAA Lys	TGA *		1437		
465						470						475						

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg
 1 5 10 15

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 20 25 30

Pro Gly Gly Ser Leu Arg Val Ser Cys Ala Val Ser Gly Phe Thr Phe
 35 40 45

Ser Asp His Tyr Met Tyr Trp Phe Arg Gln Ala Pro Gly Lys Gly Pro

50					55					60					
Glu	Trp	Val	Gly	Phe	Ile	Arg	Asn	Lys	Pro	Asn	Gly	Gly	Thr	Thr	Glu
65					70					75					80
Tyr	Ala	Ala	Ser	Val	Lys	Asp	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser
				85					90					95	
Lys	Ser	Ile	Ala	Tyr	Leu	Gln	Met	Ser	Ser	Leu	Lys	Ile	Glu	Asp	Thr
			100					105					110		
Ala	Val	Tyr	Tyr	Cys	Thr	Thr	Ser	Tyr	Ile	Ser	His	Cys	Arg	Gly	Gly
		115					120					125			
Val	Cys	Tyr	Gly	Gly	Tyr	Phe	Glu	Phe	Trp	Gly	Gln	Gly	Ala	Leu	Val
	130					135					140				
Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala
145						150					155				160
Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu
				165					170					175	
Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly
			180					185					190		
Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser
		195					200					205			
Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu
	210					215					220				
Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr
225					230					235					240
Lys	Val	Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr
				245					250					255	
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe
			260					265					270		
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro
		275					280					285			
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val
		290				295					300				
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr
305					310					315					320
Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val
				325					330					335	
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys
			340					345					350		

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 355 360 365
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 370 375 380
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 385 390 395 400
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 405 410 415
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 420 425 430
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 435 440 445
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 450 455 460
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys *
 465 470 475

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..711

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG	AGG	GTC	CCC	GCT	CAG	CTC	CTG	GGG	CTC	CTG	CTG	CTC	TGG	CTC	CCA	48
Met	Arg	Val	Pro	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Pro	
1				5				10					15			
GGT	GCA	CGA	TGT	GAG	TCT	GTC	CTG	ACA	CAG	CCG	CCC	TCA	GTG	TCT	GGG	96
Gly	Ala	Arg	Cys	Glu	Ser	Val	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Gly	
			20					25					30			
GCC	CCA	GGG	CAG	AAG	GTC	ACC	ATC	TCG	TGC	ACT	GGG	AGC	ACC	TCC	AAC	144
Ala	Pro	Gly	Gln	Lys	Val	Thr	Ile	Ser	Cys	Thr	Gly	Ser	Thr	Ser	Asn	

35	40	45	
ATT GGA GGT TAT GAT CTA CAT TGG TAC CAG CAG CTC CCA GGA ACG GCC Ile Gly Gly Tyr Asp Leu His Trp Tyr Gln Gln Leu Pro Gly Thr Ala 50 55 60			192
CCC AAA CTC CTC ATC TAT GAC ATT AAC AAG CGA CCC TCA GGA ATT TCT Pro Lys Leu Leu Ile Tyr Asp Ile Asn Lys Arg Pro Ser Gly Ile Ser 65 70 75 80			240
GAC CGA TTC TCT GGC TCC AAG TCT GGT ACC GCG GCC TCC CTG GCC ATC Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ala Ala Ser Leu Ala Ile 85 90 95			288
ACT GGG CTC CAG ACT GAG GAT GAG GCT GAT TAT TAC TGC CAG TCC TAT Thr Gly Leu Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr 100 105 110			336
GAC AGC AGC CTG AAT GCT CAG GTA TTC GGA GGA GGG ACC CGG CTG ACC Asp Ser Ser Leu Asn Ala Gln Val Phe Gly Gly Gly Thr Arg Leu Thr 115 120 125			384
GTC CTA GGT CAG CCC AAG GCT GCC CCC TCG GTC ACT CTG TTC CCG CCC Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro 130 135 140			432
TCC TCT GAG GAG CTT CAA GCC AAC AAG GCC ACA CTG GTG TGT CTC ATA Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile 145 150 155 160			480
AGT GAC TTC TAC CCG GGA GCC GTG ACA GTG GCC TGG AAG GCA GAT AGC Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser 165 170 175			528
AGC CCC GTC AAG GCG GGA GTG GAG ACC ACC ACA CCC TCC AAA CAA AGC Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser 180 185 190			576
AAC AAC AAG TAC GCG GCC AGC AGC TAC CTG AGC CTG ACG CCT GAG CAG Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln 195 200 205			624
TGG AAG TCC CAC AGA AGC TAC AGC TGC CAG GTC ACG CAT GAA GGG AGC Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser 210 215 220			672
ACC GTG GAG AAG ACA GTG GCC CCT ACA GAA TGT TCA TGA Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser *			711
225 230 235			

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp Leu Pro
 1 5 10 15
 Gly Ala Arg Cys Glu Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly
 20 25 30
 Ala Pro Gly Gln Lys Val Thr Ile Ser Cys Thr Gly Ser Thr Ser Asn
 35 40 45
 Ile Gly Gly Tyr Asp Leu His Trp Tyr Gln Gln Leu Pro Gly Thr Ala
 50 55 60
 Pro Lys Leu Leu Ile Tyr Asp Ile Asn Lys Arg Pro Ser Gly Ile Ser
 65 70 75 80
 Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ala Ala Ser Leu Ala Ile
 85 90 95
 Thr Gly Leu Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
 100 105 110
 Asp Ser Ser Leu Asn Ala Gln Val Phe Gly Gly Gly Thr Arg Leu Thr
 115 120 125
 Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro
 130 135 140
 Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile
 145 150 155 160
 Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser
 165 170 175
 Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser
 180 185 190
 Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln
 195 200 205
 Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser
 210 215 220
 Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser *
 225 230 235

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1431 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..1431

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..1431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCT CCC AGA TGG	48
Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg Trp	
1 5 10 15	
GTC CTG TCC CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG	96
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys	
20 25 30	
CCT TCG GAG ACC CTG TCC CTC ACC TGC GCT GTC TCT GGT GGC TCC ATC	144
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile	
35 40 45	
AGC GGT GGT TAT GGC TGG GGC TGG ATC CGC CAG CCC CCA GGG AAG GGG	192
Ser Gly Gly Tyr Gly Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly	
50 55 60	
CTG GAG TGG ATT GGG AGT TTC TAT AGT AGT AGT GGG AAC ACC TAC TAC	240
Leu Glu Trp Ile Gly Ser Phe Tyr Ser Ser Ser Gly Asn Thr Tyr Tyr	
65 70 75 80	
AAC CCC TCC CTC AAG AGT CAA GTC ACC ATT TCA ACA GAC ACG TCC AAG	288
Asn Pro Ser Leu Lys Ser Gln Val Thr Ile Ser Thr Asp Thr Ser Lys	
85 90 95	
AAC CAG TTC TCC CTG AAG CTG AAC TCT ATG ACC GCC GCG GAC ACG GCC	336
Asn Gln Phe Ser Leu Lys Leu Asn Ser Met Thr Ala Ala Asp Thr Ala	
100 105 110	
GTG TAT TAC TGT GTG AGA GAT CGT CTT TTT TCA GTT GTT GGA ATG GTT	384
Val Tyr Tyr Cys Val Arg Asp Arg Leu Phe Ser Val Val Gly Met Val	
115 120 125	
TAC AAC AAC TGG TTC GAT GTC TGG GGC CCG GGA GTC CTG GTC ACC GTC	432
Tyr Asn Asn Trp Phe Asp Val Trp Gly Pro Gly Val Leu Val Thr Val	
130 135 140	
TCC TCA GCT AGC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC	480
Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser	
145 150 155 160	

TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG	GGC	TGC	CTG	GTC	AAG	528
Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	
				165					170					175		
GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA	GGC	GCC	CTG	576
Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	
			180					185					190			
ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA	CTC	624
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	
		195					200				205					
TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	672
Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	
	210					215					220					
CAG	ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	720
Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	
225					230					235					240	
GAC	AAG	AAA	GCA	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	768
Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	
				245					250					255		
CCG	TGC	CCA	GCA	CCT	GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC	816
Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	
			260					265					270			
CCC	CCA	AAA	CCC	AAG	GAC	ACC	CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	864
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	
		275					280					285				
ACA	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC	GAA	GAC	CCT	GAG	GTC	AAG	TTC	912
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	
	290					295					300					
AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	960
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	
305					310					315					320	
CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC	GTC	CTC	ACC	1008
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	
				325					330					335		
GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	AAG	GTC	1056
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	
			340					345					350			
TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	1104
Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	
		355					360					365				
AAA	GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	1152
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	
	370					375					380					

GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC 1200
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 385 390 395 400

TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG 1248
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 405 410 415

GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC 1296
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 420 425 430

TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG 1344
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 435 440 445

GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC 1392
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 450 455 460

CT TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA 1431
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys *
 465 470 475

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 1 5 10 15

Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
 20 25 30

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile
 35 40 45

Ser Gly Gly Tyr Gly Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly
 50 55 60

Leu Glu Trp Ile Gly Ser Phe Tyr Ser Ser Ser Gly Asn Thr Tyr Tyr
 65 70 75 80

Asn Pro Ser Leu Lys Ser Gln Val Thr Ile Ser Thr Asp Thr Ser Lys
 85 90 95

Asn Gln Phe Ser Leu Lys Leu Asn Ser Met Thr Ala Ala Asp Thr Ala
 100 105 110

Val Tyr Tyr Cys Val Arg Asp Arg Leu Phe Ser Val Val Gly Met Val
 115 120 125
 Tyr Asn Asn Trp Phe Asp Val Trp Gly Pro Gly Val Leu Val Thr Val
 130 135 140
 Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
 145 150 155 160
 Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
 165 170 175
 Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
 180 185 190
 Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
 195 200 205
 Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
 210 215 220
 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
 225 230 235 240
 Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 245 250 255
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 260 265 270
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 275 280 285
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 290 295 300
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 305 310 315 320
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 325 330 335
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 340 345 350
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 355 360 365
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 370 375 380
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 385 390 395 400
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 405 410 415

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
420 425 430

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
435 440 445

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
450 455 460

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys *
465 470 475